



SWAMP DATA MANAGEMENT PLAN

Taxonomy Results Template

Surface Water Ambient Monitoring Program

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http://www.waterboards.ca.gov/water_issues/programs/swamp

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E. ANALYTICAL DATA

The typical method for submitting Laboratory Analytical Data to the SWAMP Database is electronically through the [online data checker](#). This section will focus on the tools and steps involved in submitting these data.

The following information should be used in conjunction with the SWAMP QAPrP for complete compliance with the SWAMP program including measurement quality objectives and required QA samples.

2. TAXONOMY ANALYSIS AUTHORIZATION FORMS

Prior to a sampling event, it is helpful to organize and identify what taxonomic samples are to be analyzed. For those organizations contracting with the Department of Fish and Game (DFG) for sampling activity, the tool used for this expectation of work is called a Taxonomy Analysis Authorization Form. This AA form is a copy of the [Taxonomy Results Template](#) (also available online) with specific samples listed for analysis.

The Analysis Authorization (AA) form is an Excel workbook provided to the labs in an electronic format prior to sampling. It is used as a detailed supplement to the Chain of Custody (COC) documentation that travels with the samples from the field to the lab. Should any discrepancy between the two types of documentation occur, contact the provider of the Analysis Authorization for further clarification.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
	Event Code	Protocol Code	Station Code	Sample Date	Agency Code	Project Code	User Name	Sample Comments	Instrument Code	Sample Stage	Collection Time	Collection Method Code	Sample Type Code	Replicate	Collection & Replicate Name
2	EXAMPLE MARINE INVERTEBRATES														
11	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	1	MPSL-MLML Mod VarV
12	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	1	MPSL-MLML Mod VarV
13	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	2	MPSL-MLML Mod VarV
14	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	2	MPSL-MLML Mod VarV
15	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	2	MPSL-MLML Mod VarV
16	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Grab	Grab	1	MPSL-MLML Mod VarV
17	WQ	MPSL-DFO_Field_v1.0	306MSL022	04Jun2004	MPSL-MLML	SWAMP_RB3	msigala	Station in deep water	Open/Water	Point	10:00	Sed_Core	Grab	1	Core_0.0071m2
18	EXAMPLE BENTHIC INVERTEBRATES														
19	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_TBC	Integrated	1	D-Frame Kick Net
20	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
21	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
22	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
23	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
24	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
25	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
26	BA	SWAMP_WVS	401VCJACL	05Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
27	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	1	D-Frame Kick Net
28	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	BW_RAB	Integrated	2	D-Frame Kick Net
29	EXAMPLE DIATOMS														
30	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	Algae_SWAMP	Integrated	1	RubDeim & PVCDeim
31	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	Algae_SWAMP	Integrated	1	RubDeim & PVCDeim
32	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	Algae_SWAMP	Integrated	1	RubDeim & PVCDeim
33	BA	SWAMP_WVS	401VOMADL	07Jun2006	MPSL-DFO	SWAMP_RB4	admin		X	Point	11:00	Algae_SWAMP	Integrated	1	RubDeim & PVCDeim

- The **BenthicCollectionResults** worksheet provides the sample information in the correct template format for the laboratory to use in order to enter the analysis results.
- A **BenthicCollectionResults Example** worksheet is also listed which gives an example of the final formatting of the taxonomy template.

Regardless of whether an organization chooses to use these Analysis Authorization Forms or others like them that serve the same purpose, they are useful tools to help communicate and maintain consistency



regarding samples collected and analyzed. If interested, contact the SWAMP DMT to receive an electronic version of an AA form template.

7. TAXONOMIC DATA

Data for marine benthic infauna, freshwater benthic macroinvertebrate (BMI), algae, and diatom taxonomic analyses are treated in a similar way in the SWAMP database and for this reason will be treated together in this portion of the document.

a. Taxonomy Results Template

The Taxonomy Results Template is available online at <http://swamp.mpsl.mlml.calstate.edu/resources-and-downloads/database-management-systems/swamp-25-database/templates-25#Taxonomic>.

b. Formatting the Data

A Microsoft Excel template exists for laboratories to use to format and submit taxonomy results in a manner that can be easily loaded into the SWAMP database. As previously discussed, for many labs working under the SWAMP master contract, the station collection information can be obtained from the Taxonomy Analysis Authorization form. This section will discuss each of the fields in the template and how to populate them.

All valid LookUp list values are available at http://checker.swamp.mpsl.mlml.calstate.edu/SWAMP_Checker/LookUpLists.php. If the necessary field and/or values do not appear in the LookUp list, a request to have it added can be submitted to the SWAMP Data Management Team (DMT).



i. Benthic Collection Results Worksheet

There is one worksheet that must travel with the data for the data package to be considered complete. This worksheet holds all marine benthic infauna, freshwater benthic macroinvertebrate (BMI), algae, and diatom collection and result data, and should be named **BenthicCollectionResults** in a worksheet tab. Each record in this sheet represents a unique taxonomic identification from each sample and collection event. If beginning with a Taxonomy Analysis Authorization form, the following fields will likely be pre-populated in the **BenthicCollectionResults** worksheet: *EventCode*, *ProtocolCode*, *StationCode*, *SampleDate*, *AgencyCode*, *ProjectCode*, *LocationCode*, *CollectionTime*, *CollectionMethodCode*, *SampleTypeCode*, *Replicate*, *CollectionDeviceName*, *SieveSize*, *CollectionDepth*, and *UnitCollectionDepth*. Please note that all fields are required to have data except when otherwise noted below. Examples of special types of samples are listed in the [Special Circumstances](#) section.

Template Field Name	LookUp List	Description & Business Rules
StationCode	<u>StationLookUp</u>	<p>StationCode represents a unique sampling site in a sampling design. A single waterbody may have multiple stations.</p> <p>BR: StationCode should represent a geographic location not a geographic location combined with a replicate reference. There cannot be multiple StationCodes in the StationLookUp with the same target latitude/longitude coordinates.</p> <p>The format for the unique alphanumeric description of the station is ###ABC123, where ### is the Hydrologic Unit number and ABC123 is an alphanumeric description of the Station. An example is 111EELBRN which is Hydrologic Unit 111 and an abbreviated code to indicate "Eel River - South Fork near Branscomb".</p> <p>If the exact Hydrologic Unit is not known, populate the first number with the regional board number; i.e. the station is known to be in California Regional Water Board 3, the StationCode would be 300#####. If the station is not in California, the Hydrologic Unit is 000.</p>



Template Field Name	LookUp List	Description & Business Rules
SampleDate		<p>SampleDate refers to the date the sample was collected in the field.</p> <p>BR: The format for date in the templates is dd/mmm/yyyy, such as 10/Nov/2007. For samples with collection times that last longer than one day, like autosamplers, the sample date is the date sampling began.</p> <p>When entering data using the forms, the format is mm/dd/yy.</p> <p>For transplanted bivalves, the SampleDate is the date the transplanted organisms were collected, removed, or retrieved from the field.</p>
ProjectCode	<u>ProjectLookUp</u>	<p>ProjectCode is a unique code referencing a project which includes data of a single study design; e.g. RWB5_StS_FY0708, RWB2_Status_YR1, RWB7_Trend_2003, SWB_RCMP_2008.</p> <p>BR: ProjectCodes with FY in the name indicate samples were collected in a fiscal year calendar cycle, e.g. FY0708 would indicate fiscal year 2007-2008 which is July 1, 2007 through June 30, 2008. ProjectCodes without FY indicate samples were collected in a calendar year, e.g. 2003 would indicate calendar year 2003 which is January 1, 2003 through December 31, 2003. Each Project must have an associated QAPrP or Project QAPP listed. SWAMP moves data to the permanent side of the database by ProjectCode.</p>



Template Field Name	LookUp List	Description & Business Rules
EventCode	<u>EventLookUp</u>	<p>EventCode represents the initial intent of the sampling event at a particular station.</p> <p>BR: The EventCode will be in a hierarchical order as follows:</p> <p>BA – If the initial intent of sampling is for Bioassessment (PHab, BMI [freshwater], and/or Algae) (Tissue and/or WaterQuality samples may or may not also be collected)</p> <p>TI – If the initial intent of sampling is for Tissue (WaterQuality samples may or may not also be collected; no associated Bioassessment samples collected)</p> <p>WQ – If the initial intent of sampling is for WaterQuality (Water, Sediment, Toxicity, and/or Marine Benthic Abundance) (no associated Bioassessment or Tissue samples collected)</p> <p>For example, if the initial intent of sampling on Day 1 was for Tissue and WaterQuality, the EventCode would be TI. If for some reason the WaterQuality had to be re-sampled the next day, on Day 2, the event for the re-sampling would still be TI because Tissue was the initial intent of sampling on Day 1 even though WaterQuality was sampled on Day 2.</p>



Template Field Name	LookUp List	Description & Business Rules
ProtocolCode	<u>ProtocolLookUp</u>	<p>ProtocolCode represents the sampling protocol used, which includes the set of methods, methodology, and/or specifications; e.g. MPSL-DFG_Field_v1.0 or SWAMP_WS_2007. Established protocols may be used or Regions may document their own sampling protocols.</p> <p>BR: It is preferable to combine protocols per StationCode and date so that all WaterQuality, Bioassessment, and Tissue data are combined under the same EventCode and Protocol. For example, if Tissue and WaterQuality are sampled at a station, the EventCode would be TI. If the protocols are different for Tissue and WaterQuality, the Tissue protocol would be used and the WaterQuality protocol would be listed in the SampleComments. If that is not preferable, separate EventCodes may be used with each individual protocol.</p> <p>Not Recorded is only used for historic data. All non-historic SWAMP projects require a true protocol reference. Not Applicable is used for LABQA and 000NONPJ samples only.</p>
AgencyCode	<u>AgencyLookUp</u>	<p>AgencyCode refers to the organization or agency that collected the sample. This should be listed on the Chain of Custody (COC) document that accompanies the samples from the field.</p> <p>BR: If an environmental sample is used to perform laboratory QC, i.e. a matrix spike or lab duplicate, the AgencyCode still refers to the agency that collected the native sample, not the agency that created the QC sample.</p> <p>See 'Special Circumstances' for LABQA business rules.</p>
SampleComments (Not Required)		<p>SampleComments records any comments related to the sampling event at a particular station.</p> <p>BR: When a PurposeFailureCode of Other is used, a SampleComment is required.</p>



Template Field Name	LookUp List	Description & Business Rules
LocationCode	<u>LocationLookUp</u>	<p>LocationCode describes the physical location in the waterbody where the sample was collected. One sampling event may have a single or multiple locations.</p> <p>BR: For a single point of sampling, the physical location in the waterbody can be used such as Bank, Thalweg, Midchannel, OpenWater, Transect 1, or X (general location for bioassessments).</p> <p>For field results, the LocationCode should be the same as the location for the WaterQuality collection method.</p> <p>For TI EventType sampling, the physical location plus the CollectionMethod is used such as BankNet1, BankShock1, OpenWaterTrawl1, OpenWaterNet1. For resident mussel or clam collections, the LocationCode would be the physical location in the water body plus the generic CollectionMethod, e.g. BankTissue_Grab1.</p> <p>OpenWater sampling with multiple sub-locations within a single water body or station could have locations of OpenWaterTrawl1, OpenWaterTrawl2 describing one large location with two smaller areas of sampling within the OpenWater Location.</p> <p>Multiple physical locations within a single station could consist of a LocationCode such as BankShock1, BankNet1, OpenWaterHook1.</p> <p>If recording specific locations within a station are necessary for the project, a LocationCode such as Location1Net1, Location1Net2, Location2Shock1 may be used.</p>
GeometryShape (Not Required)	<u>VariableCodesLookUp</u>	<p>GeometryShape is the physical shape of the location; e.g. Line, Point, Line Centroid, Polygon, Polygon Centroid.</p>



Template Field Name	LookUp List	Description & Business Rules
CollectionTime		<p>CollectionTime refers to the time when the first field measure of a sampling event at a specific station was recorded in the field.</p> <p>BR: If the sampling crew collects 18 field measurements at a single station, the CollectionTime for each would be the time of the first measurement recorded. By doing so, the samples can easily be linked and any holding time issues will be consistent, and conservative, for laboratory work.</p> <p>The CollectionTime format should be expressed as xx:xx in 24 hour time, such as 13:30 for 1:30 pm.</p>
CollectionMethodCode	<u>CollectionMethodLookUp</u>	<p>CollectionMethodCode refers to the general method of collection.</p> <p>BR: For BA EventCodes, use the appropriate CollectionMethodCode for BMIs (e.g., BMI_RWB, BMI_CSBP) and for Algae (e.g., Algae_SWAMP, Algae_EMAP) that follows the associated protocol.</p> <p>The SWAMP marine invertebrates default is Sed_Grab.</p>
SampleTypeCode	<u>SampleTypeLookUp</u>	<p>SampleTypeCode refers to the type of sample collected or analyzed.</p> <p>BR: Some commonly used SampleTypeCode choices include Grab, Integrated, Macroalgae, Microalgae, Epiphyte, Qualitative, etc.</p> <p>When laboratories report soft algae taxonomy data with multiple sample types (Epiphyte, Macroalgae, Microalgae, Integrated, Qualitative), a comment should be added to the BenthicCollectionComment identifying if no taxonomic results were found for any or all of the SampleTypeCodes. It is the data submitter's responsibility to update the BenthicCollectionComment for this particular SampleTypeCode where no results were found and to notify the data loader of the change. The submitting laboratory should not delete the SampleType row from the MS Excel file.</p>



Template Field Name	LookUp List	Description & Business Rules
Replicate		Replicate is the collection replicate number used to distinguish between replicates created at collection. BR: If a replicate was performed in the lab, indicate replicate 2 and make a comment in the BenthicCollectionComments that it was a lab replicate.
CollectionDeviceName	<u>CollectionDeviceLookUp</u>	CollectionDeviceName refers to the specific device used in the collection of the sample such as MPSL-MLML Mod.VanVeen Grab-DbI_0.05m2, 0.05m2 or Core_0.0071m2 for marine invertebrate collections, D-Frame Kick Net for BMI invertebrate collections, and RubDelim & PVCDelim or Individual Collection by Hand for algae and diatom collections.
SieveSize	<u>VariableCodesLookUp</u>	SieveSize is the size of the sieve the sample was passed through; e.g. 0.5mm, none
CollectionDepth		CollectionDepth records the level, from the surface in the water or sediment column, at which the field measurements were recorded. BR: This information should be listed on the field data sheet from the field crew. CollectionDepth for water samples would be measured from the water surface and recorded in meters (m). Since depths for ambient monitoring field measurements are generally "subsurface", defaults have been established to indicate this. For water samples, the default value is 0.1 m. For freshwater bioassessments, algae, and diatom samples where samples are composited, the default is -88 m. If samples were composited from multiple locations at different depths, CollectionDepth is -88.
UnitCollectionDepth	<u>VariableCodesLookUp</u>	UnitCollectionDepth refers to the units used in the CollectionDepth including cm (centimeters) and m (meters). This information should be listed on the Chain of Custody (COC) document that accompanies samples from the field.



Template Field Name	LookUp List	Description & Business Rules
SampleID (Not Required)		<p>SampleID is a unique identifier supplied by the organization directing the sampling or sampling agency and is used to track the sample throughout the sampling and analysis processes. This field can be used to tie a result to the sample.</p> <p>BR: This SampleID, which is different from the StationCode, will likely be on the sample container the laboratory receives from the field crew or on the COC. If there is no number, leave this field blank.</p>
BenthicCollectionComments (Not Required)		<p>BenthicCollectionComments records any comments relating to the collection of the field sample for laboratory analysis.</p> <p>BR: If no results were found, enter a comment stating that no organisms were identified. If a sample collection is missing an expected bottle, or the bottle broke or was lost enroute to or at the laboratory, enter a comment here describing why results are not reported. The submitting laboratory should not delete the sample row from the MS Excel file in either situation.</p>
GrabSize (Not Required)		<p>GrabSize is the total area of substrate collected for the sample, regardless of CollectionDevice area size. This is determined by the sampling device area and, if applicable, the number of transects or grabs sampled.</p>
UnitGrabSize (Not Required)	<u>VariableCodesLookUp</u>	<p>UnitGrabSize refers to the units used for GrabSize; from UnitGrabSizeList in VariableCodesLookUp; e.g. m2 or cm2.</p>
ReplicateName (Not Required)		<p>ReplicateName is the name of the Replicate Number if applicable; e.g. Transect 1 or T-1. This field was used previously in the CalEDAS database to identify if replicate samples were collected.</p>
ReplicateCollectionDate (Not Required)		<p>ReplicateCollectionDate is the date of the ReplicateCollection; format as dd/mmm/yyyy</p>
NumberJars (Not Required)		<p>NumberJars is the number of jars into which the sample fit for transport to the analytical lab</p>
BenthicCollectionDetailComments (Not Required)		<p>BenthicCollectionDetailComments are comments related to the BenthicCollectionDetail</p>



Template Field Name	LookUp List	Description & Business Rules
AgencyCode_LabEffort	<u>AgencyLookUp</u>	AgencyCode_LabEffort is the agency that sorted or processed the taxonomic sample
PersonnelCode_LabEffort	<u>PersonnelLookUp</u>	PersonnelCode_LabEffort refers to the Lab personnel (sorter or taxonomist) who processed the sample, performed the initial sorting of the sample, and was responsible for this entry.
PercentSampleCounted (Not Required)		PercentSampleCounted refers to the percent of the sample that was counted.
TotalGrids (Not Required)		TotalGrids is the total number of grids onto which the sample was spread for subsampling.
GridsAnalyzed (Not Required)		GridsAnalyzed is the number of grids (in integers) of material pulled from to achieve the TargetOrganismCount.
GridsVolumeAnalyzed (Not Required)		Volume of grids included in the analysis required to achieve the TargetOrganismCount; i.e. if 0.25 from each of 3 grids were analyzed, GridsVolumeAnalyzed would be 0.75. Units are in grids.
TargetOrganismCount (Not Required)		TargetOrganismCount is the number of organisms at which subsampling will cease.
ActualOrganismCount (Not Required)		ActualOrganismCount is the total number of organisms recovered by lab sorter in all grids analyzed, including the count above and beyond the target total for the subsample.
ExtraOrganismCount (Not Required)		ExtraOrganismCount is the number of organisms subsampled beyond the target count.
QCOrganismCount (Not Required)		QCOrganismCount refers to the number of organisms in the subsample counted during the quality control (QC) check. It refers to cases where a sample is re-sorted and more organisms are found. If the original sort found 500 organisms and then it was re-sorted by a different person who found 3 organisms, the QCOrganismCount would be 3 rather than 503.
DiscardedOrganismCount (Not Required)		DiscardedOrganismCount is the number of organisms in the subsample determined to be unsuitable for identification.



Template Field Name	LookUp List	Description & Business Rules
EffortQACode	<u>EffortQALookUp</u>	EffortQACode is a unique code applied to the result which describes any special conditions, situations or outliers occurring during or prior to lab sorting.
BenthicLabEffortComments (Not Required)		BenthicLabEffortComments are the comments related to lab sorting or sample processing.
FinalID	<u>OrganismLookup</u>	FinalID refers to the lowest taxon level identified for the organism.
LifeStageCode	<u>LifeStageLookUp</u>	LifeStageCode is a unique code referencing the stage of life of the organism; e.g. adult, juvenile, larvae.
Distinct		Distinct is an indicator of whether this is a distinct (≥ 1) or non-distinct (0) taxon.
BAResult		<p>BAResult is the number of individuals of a given FinalID and stage that were identified within a sample replicate. This is for unadjusted (raw) counts and is to be used for cases where a TargetOrganismCount is used.</p> <p>Either BAResult or Result should be populated (unless QACodes and ResQualCodes other than the defaults are used), but NOT both fields.</p>
Result		<p>Result is the final numeric result of a given FinalID and stage scaled up to grab size. Result is for counts adjusted to the area sampled and for biovolumes and it may represent raw counts if the full sample is sorted.</p> <p>BR: Either BAResult or Result should be populated (unless QACodes and ResQualCodes other than the defaults are used), but NOT both fields.</p>
UnitName	<u>UnitLookUp</u>	<p>UnitName refers to how the taxonomic result is measured or expressed.</p> <p>BR: Taxonomic units are indicated by count or volume/area, e.g. $\mu\text{m}^3/\text{cm}^2$</p>



Template Field Name	LookUp List	Description & Business Rules
ResQualCode	<u>ResQualLookUp</u>	<p>ResQualCode or Result Qualifier Code qualifies the analytical result of the sample.</p> <p>BR: This field should have an equal sign (=) for results that are recorded. When a result is Greater Than (>) or Less Than (<), a ResQualCode is required and the appropriate code would be applied.</p> <p>When both the BAREsult and Result are blank, a ResQualCode is required. If the ResQualCode value is NR for Not Recorded, then a reason for this code must be written in the BenthicResultComments field and/or an appropriate QACode would be applied.</p>
QACode	<u>QALookUp</u>	<p>QACode is applied to the result to describe any special conditions, situations or outliers that occurred during or prior to the identification to achieve the result.</p> <p>BR: The default code, indicating no special conditions, is None. If more than one code should be applied to a record, the convention is to list them in alphabetical order separated by commas and no spaces; e.g. GB,SC.</p>
ComplianceCode	<u>ComplianceLookUp</u>	ComplianceCode is a unique code referencing the Compliance with the associated QAPP.
BatchVerificationCode	<u>BatchVerificationLookUp</u>	BatchVerificationCode is a unique code referencing the Verification of a Batch.
TaxonomicQualifier (Not Required)	<u>VariableCodesLookUp</u>	TaxonomicQualifier is a code representing the taxonomist's justification for not identifying a specimen to standard effort; from TaxonomicQualifierList in VariableCodesLookUp.
ExcludedTaxa (Not Required)	<u>VariableCodesLookUp</u>	ExcludedTaxa is a code representing the taxonomist's justification for excluding a specimen from analysis; from ExcludedQualifierList in VariableCodesLookUp.



Template Field Name	LookUp List	Description & Business Rules
PersonnelCode_Result	<u>PersonnelLookUp</u>	<p>PersonnelCode_Result is a unique code referencing the personnel or person who performed the taxonomy and produced the FinalID.</p> <p>In some cases, the PersonnelCode_LabEffort and PersonnelCode_Result are the same person. In other cases, the lab pays a student to do the initial sorting of pulling organisms out of the sample (PersonnelCode_Lab Effort) and then has a taxonomist do the actual identification (PersonnelCode_Results).</p>
LabSampleID (Not Required)		LabSampleID is a recommended field intended to provide lab specific identification for an analyzed sample. The format and content is determined by the lab.
EnterDate (Not Required)		EnterDate is the date the data were entered into the template; formatted as dd/mmm/yyyy.
BenthicResultComments (Not Required)		BenthicResultComments are comments related to the BenthicResult or individual taxa count.



c. *Special Circumstances*

There are two types of special circumstances discussed in this section. SWAMP is currently developing QA/QC guidance for freshwater bioassessment taxonomy.

(a) Qualitative Organism Identifications

Qualitative organism identifications refer to samples where the field personnel note the presence of algae in the stream without noting the abundance of the taxon. The special circumstances for recording these types of results are as follows:

<i>SampleTypeCode</i>	Qualitative
<i>Result</i>	Leave null
<i>ResQualCode</i>	P (present)
<i>Unit</i>	count

(b) Colonial Organism Counts

Colonial organism counts refer to samples where the objective is to obtain a count for a taxon but a colonial organism is found. Laboratories should not provide a count in these cases due to the difficulty in obtaining a count for certain organism types (e.g. a sponge or hydroid). If a biovolume or biomass is the objective, then record the result and appropriate unit. The special circumstances for recording colonial organism counts are as follows:

<i>SampleTypeCode</i>	Epiphyte, Macroalgae, etc. (not Qualitative)
<i>Result</i>	Leave null
<i>ResQualCode</i>	COL (Colonial)
<i>Unit</i>	count

d. *Procedure for Adding New Organisms to the Database*

There are instances when new organisms will need to be added to the SWAMP database. Following is the procedure to add those organisms.

i. Adding a New Organism

The first step is to check the OrganismLookUp list online http://checker.swamp.mpsl.milml.calstate.edu/SWAMP_Checker/LookUpLists.php to determine if the organism already exists in the list. If the organism does not exist in SWAMP, the name and associated information must be submitted to the SWAMP DMT for consideration to be added to the database. Additional information may be found through [SCAMIT](#) for marine taxonomic references and [SAFIT](#) for freshwater taxonomic references.



ii. Organism_DetailLookup Worksheet

Once it is determined that an organism is not in the current lookup list, complete the Organism_DetailLookup worksheet in the [SWAMP Taxonomy Results Template](#). Please note that all fields are required to have data except when otherwise noted below, but it is preferred to populate all fields if the information is known. In cases where an organism has multiple LifeStageCodes, a record consisting of each FinalID and LifeStageCode combination would be expected.

Template Field Name	LookUp List	Description & Business Rules
CommonName (Not Required)		CommonName refers to the common name of the organism collected.
FinalID		FinalID is the lowest taxon level identified for the organism. BR: Do not use sp. or spp. after the genus name as part of the FinalID if the organism can only be identified down to the genus and not the species. It is allowable if the organism is known as Genus sp A, where Species A is a known and documented species.
ParentFinalID (Not Required)		ParentFinalID is the FinalID of the parent Taxon ID.
Phylum		Phylum is the phylum of the organism; a taxonomic rank used in the classification of organisms.
Subphylum (Not Required)		Subphylum is the subphylum of the organism; a taxonomic rank used in the classification of organisms.
Superclass (Not Required)		Superclass is the superclass of the organism; a taxonomic rank used in the classification of organisms.
Class		Class is the class of the organism; a taxonomic rank used in the classification of organisms.
Subclass (Not Required)		Subclass is the subclass of the organism; a taxonomic rank used in the classification of organisms.
Superorder (Not Required)		Superorder is the superorder of the organism; a taxonomic rank used in the classification of organisms.



Template Field Name	LookUp List	Description & Business Rules
Order		Order is the order of the organism; a taxonomic rank used in the classification of organisms.
Suborder (Not Required)		Suborder is the suborder of the organism; a taxonomic rank used in the classification of organisms.
Superfamily (Not Required)		Superfamily is the superfamily of the organism; a taxonomic rank used in the classification of organisms.
Family		Family is the family of the organism; a taxonomic rank used in the classification of organisms.
Subfamily (Not Required)		Subfamily is the subfamily of the organism; a taxonomic rank used in the classification of organisms.
Tribe (Not Required)		Tribe is the tribe of the organism; a taxonomic rank used in the classification of organisms.
GenusComplex (Not Required)		GenusComplex is the genus complex of the organism; a taxonomic rank used in the classification of organisms.
Genus		Genus is the genus of the organism; a taxonomic rank used in the classification of organisms.
SpeciesComplex (Not Required)		SpeciesComplex is the species complex of the organism; a taxonomic rank used in the classification of organisms.
Species		Species is the species of the organism; a taxonomic rank used in the classification of organisms.
Subspecies		Subspecies is the subspecies of the organism; a taxonomic rank used in the classification of organisms.
Variety (Not Required)		Variety is the variety of the organism; a taxonomic rank used in the classification of organisms.
TaxonomicLevelCode	<u>TaxonomicLevelLookup</u>	TaxonomicLevelCode is a unique code referencing the level of the FinalID.



http://www.waterboards.ca.gov/water_issues/programs/swamp

Template Field Name	LookUp List	Description & Business Rules
LifeStageDefault	<u>LifeStageLookUp</u>	LifeStageDefault is the default LifeStageCode of each organism or FinalID one expects to find and to be used in analyses. BR: Default value is NR.
TaxonomicAuthority (Not Required)		TaxonomicAuthority is the Taxonomist or reference (including year) used to identify the organism; e.g. Barnum 1905. BR: If the FinalID is defined to genus and species, a TaxonomicAuthority is required. If it is defined to the family level or higher, this field may be left blank if not applicable.
CaliforniaTaxon (Not Required)		CaliforniaTaxon is a yes/no field used to record if the organism is a CaliforniaTaxon, i.e. that it exists in California regardless if it exists in other states or not. BR: Limit values to TRUE or FALSE where TRUE identifies the FinalID as a California taxon.
DateFinalIDRevised (Not Required)		DateFinalIDRevised is the date the FinalID was revised. BR: Format is dd/mmm/yyyy.
FinalIDAuthority	<u>AgencyLookUp</u>	FinalIDAuthority represents the Agency that has the authority to change values for the FinalID; e.g. SAFIT, SCAMIT.
Source (Not Required)	<u>AgencyLookUp</u>	Source is the agency that introduced or added the organism to the database; e.g. MPSSL-MLML, DFG-ABL, SFEI.
OrganismComments (Not Required)		OrganismComments are comments related to the organism.
LifeStageCode	<u>LifeStageLookUp</u>	LifeStageCode is a unique code referencing the stage of life of the organism; e.g. adult, larvae. Each FinalID can have multiple yet different LifeStageCodes to create unique records; i.e. one FinalID can have both an adult and larvae LifeStageCode but not two adult LifeStageCodes.



iii. Submit Data to SWAMP

Submit taxonomic results and new LookUp values to SWAMP by following the [Submitting Data To SWAMP Data Management Team](#) procedures and using the Online Data Checker.

iv. Authority Check

Proposed new organisms will be forwarded to SCCWRP who will then forward it to the appropriate authority (e.g. SAFIT or SCAMIT) for review and consideration to be added to the SWAMP database. Follow-up questions or comments may be needed before final resolution is completed.

v. Clarification of New Organisms

If the authority has questions about the new organism, SCCWRP will be contacted. SCCWRP will then contact the SWAMP DMT who will contact the submitting laboratory to obtain the answers. This information will be relayed back to the appropriate authority for final approval of the new organism.

vi. Addition of New Organisms

Once the authority approves the new organism for addition to the SWAMP database, SCCWRP will be notified. SCCWRP will then notify the SWAMP DMT. The SWAMP DMT will then add the new organism to the SWAMP database.

